

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/502,351
Source: Pg 110
Date Processed by STIC: 3/13/05

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PCT

RAW SEQUENCE LISTING

DATE: 03/13/2005

PATENT APPLICATION: US/10/502,351

TIME: 12:06:41

Input Set : A:\2977-154 Sequence Listing.ST25.txt

Output Set: N:\CRF4\03132005\J502351.raw

```

3 <110> APPLICANT: Zhang, Lian Hui
4       Lin, Yi Han
5       Xu, Jin Liang
7 <120> TITLE OF INVENTION: Ralstonia AHL-Acylase Gene
9 <130> FILE REFERENCE: 2977-154
11 <140> CURRENT APPLICATION NUMBER: 10/502351
12 <141> CURRENT FILING DATE: 2004-07-23
14 <150> PRIOR APPLICATION NUMBER: PCT/SG02/000011
15 <151> PRIOR FILING DATE: 2002-01-23
17 <160> NUMBER OF SEQ ID NOS: 7
19 <170> SOFTWARE: PatentIn version 3.3
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 3743
23 <212> TYPE: DNA
24 <213> ORGANISM: Ralstonia sp.
27 <220> FEATURE:
28 <221> NAME/KEY: misc_feature
29 <222> LOCATION: (16)..(16)
30 <223> OTHER INFORMATION: n is a, c, g, or t
32 <400> SEQUENCE: 1
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37 cgccggaagg cggacatgtc gtgataaccg cactgttcgg cgattgccgt caggctcagc      180
39 gtgctgactt ccagcaggtg gcaggcgcgc tccacgcgca gccggtgcag caattgcagc      240
41 ggcgaggtgc ccagggtctt ggtgaaatgc cgcagcagcg tgcgtcgtc ggtcagaggc      300
43 gcggcgccca gcttggccag gtgcgaacggc tcgtgcaggt gctgctgcag gtacgcgcgc      360
45 gcccgcagta ccacgctggc gcggatggcg ggcttgctgc gcagccagat ggcggtggac      420
47 tcaccgcgcg acgggtggc gagcacggcc tggccgaggg tgcgtgccag ccgggtgtcg      480
49 gccaggcggc cgaccaggcg ctgcgtgagc gccacgcctg gctccatcgc gcgcgcgcgc      540
51 agcacgttgc cgctgctgac gatggcctgc tccgccacca ccttcagctg cgggtagtgt      600
53 ccgtgcagcc agccggcgat cagccacgtc accgtcaagc gccggccggc gggcagcgcg      660
55 ccggccagca gcgccacgcc ggtgaaggac gagggccacca agcctgccgg cgtccaggta      720
57 gcgcgggatg gtggcgcgct cccactccag caggggccagg cgctgctcca gcgtgctgat      780
59 gtggtcgaaa tgcagggggc ggacgaccag cgcgtcgccc agcgcggcgt cggccgcgg      840
61 cagcggtcgg cagcggcagg ccagggtctc ggccggcgcc tgcagcggg ccgggtcgcg      900
63 cgcgaccagc cgcaccccca acaccgggct ggccggcatc gcacgcttgc cggcatgcat      960
65 ggaggcgagc gcattggcca cgcgaggggt gtcggcgacg gtcgccagcg tggagaggcc      1020
67 ggcgtcggga aaggtcagca ggtcgatgtc ggcattccga aagtataggg gaggcggggc      1080
69 gaggcctcct gcgtggcggg attgacccca actctggcgg gaatacctct ttctccggg      1140
71 cgggccccag tcgacgatac ggcggtggct gcgcctgcgc gccgcgcgaa gactagagcg      1200
73 acacaagaca agaccgacaa caggagacaa cgcattgatc agggattcgc gctgcgcggc      1260
75 acgctcgcca tggccgcgct cgcggcgctg gccggctgcg ccagttccac cgatggcgcg      1320
77 tgggggtcgc tcagcgacac cggcctgtcc gccgagatcc gccgcaccgg cttcggcatt      1380

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79 ccgcacatcc gcgccaacga ctacgccagc ctcggtatg gcattggccta tgcctacgcg 1440
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83 accttcgggc ccgagggcac cgtgacggtc tcgttcaagc cgatcccaa cctgcagtcg 1560
85 gacgccttct tcaagggcat cttcgacgag gacggcctgc gcgcgggta tgcgcagatg 1620
87 tcgcccagag cgcgcgagct gctgcgcggc tacatcgccg gcttcaaccg ctatctcaag 1680
89 gacacgcgcg ccgccaactt cccggccgcc tgcgcgaatg ccgcctgggt gcgtccgctc 1740
91 acgctgggcg acatgatgcg catggggcga gagaaggcga tccaggccag cgcggcgcc 1800
93 atgctggcgg gcacgtgcg cgcgacggc cggggccgca cgccggtggc cgagcgcgag 1860
95 attccgcgcg aggcgctcga caccgtggcg ctggaccgcg aactgcagct gcgcgacatg 1920
97 ccgatcggct ccaacggctg ggccttcggc gctgacgcca ccgccaaccg gcgcggcgctg 1980
99 ctgctcggca atccgcactt cccgtggacg accaccaacc gcttctacca ggtccacctg 2040
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103 atcggcttca acaaggacgt ggcgtggacg cacaccgtct ccaccggccg ccgcttcacc 2160
105 ttgttcgaac tgaagctggc cgaaggcgac ccgaccacct acctggtcga cggcacgcgcg 2220
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109 cgccgcacgc acaccttcta cgacaccatc tacggcccgg tgcgtgcgat gccgagcggc 2340
111 ggcatgccgt ggaccacgca gaaggcctac gccctgcgcg acgccaaccg caacaacacg 2400
113 cgctcggctg acagctggct gcatacggg caggcccggg acgtggccgg catccgccag 2460
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117 gcgctgttcg cgcagctgtc gaccacggc gacgtgccgg ccgcggagct ccagcgtgt 2580
119 gccccgtcgc cgtggccgg caaactcttc aaggacgcgg gcctggtgct gctcgacggc 2640
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123 cccgcgcgca tgccgggtgt cgagcgcgac gactacgtcg ccaacagcaa tgacagctcc 2760
125 tggtgacca acccgcgcga aaagctgacc ggcttctcgc cggatgatgg ctcggtcgac 2820
127 gtaccgcagc ggctgcgcac gcgcacggc ctgategaga tcggccgcgg cctggccggc 2880
129 accgacggac tgcccggcaa ccgcacgat ctgccgaacc tgcaggcgat gatcttcagc 2940
131 aatgccaaac tggcgggaca actggtgctg ggcgacctgc tcgcggcatg caaggccacg 3000
133 ccggcccccg atgccgacgt gcgcgacggc tgcgcgcgcc tcggccagtg gaaccgcacc 3060
135 agcaacgcgg acgcccgcgc cgcgcacctg ttccgcgagt tctggatgcg cgccaaggac 3120
137 atcgcgcagg tgcacgccgt cgagttcgac ccggccgacc cgggtccacac gccgcgcggc 3180
139 ctgcgcgatg acgacgcgac ggtacgcacg gcggtgttca aggcgctgaa ggaagccgtg 3240
141 ggcgcgggtg gcaaggcggg cttcgcgctg gatgcgcgcg tgggcacggg acaggccgcg 3300
143 cacgcaccgg acggctccat cgccctgcac ggcggcgagg aatacgaagg cgtgctcaac 3360
145 aagctgcaaa ccctgccgat cgggcggaag gggctgcggg tgtatttcgg caccagctac 3420
147 atccagaccg tgaccttcga cgaccagggc ccggtcgccg acgccatcct cacctacggc 3480
149 gaatcgaccg accacgcctc gccgcacgcy ttcgaccaga tgcgtgcgta ctcgggcaag 3540
151 cactggaacc ggctgccgtt ctccgaagcg gccatcgcg cccgatccggc gctgaagggtg 3600
153 atgcgggtgt cgcagtgagg gctgcgggtg cctggaaaaa cgcgccgctt gtgcggggcg 3660
155 tttttttgcc agtgtgaatg gctcaatcgt gttggaaacc gcacccggac atgactgtat 3720
157 tgtgactctg cctgtgtccg tgt 3743
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 794
162 <212> TYPE: PRT
163 <213> ORGANISM: Ralstonia sp.
165 <400> SEQUENCE: 2
167 Met Met Gln Gly Phe Ala Leu Arg Gly Thr Leu Ala Met Ala Ala Leu
168 1 5 10 15
171 Ala Ala Leu Ala Gly Cys Ala Ser Ser Thr Asp Gly Arg Trp Gly Ser
172 20 25 30

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175 Leu Ser Asp Thr Gly Leu Ser Ala Glu Ile Arg Arg Thr Gly Phe Gly
176      35      40      45
179 Ile Pro His Ile Arg Ala Asn Asp Tyr Ala Ser Leu Gly Tyr Gly Met
180      50      55      60
183 Ala Tyr Ala Tyr Ala Gln Asp Asn Leu Cys Leu Leu Ala Asp Gln Val
184 65      70      75      80
187 Val Thr Val Asn Gly Glu Arg Ser Lys Thr Phe Gly Pro Glu Gly Thr
188      85      90      95
191 Val Thr Val Ser Phe Lys Pro Ile Pro Asn Leu Gln Ser Asp Ala Phe
192      100     105     110
195 Phe Lys Gly Ile Phe Asp Glu Asp Gly Leu Arg Ala Gly Tyr Ala Gln
196      115     120     125
199 Met Ser Pro Glu Ala Arg Glu Leu Leu Arg Gly Tyr Ile Ala Gly Phe
200      130     135     140
203 Asn Arg Tyr Leu Lys Asp Thr Pro Pro Ala Asn Phe Pro Ala Ala Cys
204 145     150     155     160
207 Arg Asn Ala Ala Trp Val Arg Pro Leu Thr Leu Gly Asp Met Met Arg
208      165     170     175
211 Met Gly Glu Glu Lys Ala Ile Gln Ala Ser Ala Gly Ala Met Leu Ala
212      180     185     190
215 Gly Ile Val Ala Ala Gln Pro Pro Gly Arg Thr Pro Val Ala Glu Arg
216      195     200     205
219 Glu Ile Pro Pro Gln Ala Val Asp Thr Val Ala Leu Asp Arg Glu Leu
220      210     215     220
223 Gln Leu Arg Asp Met Pro Ile Gly Ser Asn Gly Trp Ala Phe Gly Ala
224 225     230     235     240
227 Asp Ala Thr Ala Asn Arg Arg Gly Val Leu Leu Gly Asn Pro His Phe
228      245     250     255
231 Pro Trp Thr Thr Thr Asn Arg Phe Tyr Gln Val His Leu Thr Val Pro
232      260     265     270
235 Gly Lys Leu Asp Val Met Gly Ala Ser Ile Ala Ala Phe Pro Val Val
236      275     280     285
239 Ser Ile Gly Phe Asn Lys Asp Val Ala Trp Thr His Thr Val Ser Thr
240      290     295     300
243 Gly Arg Arg Phe Thr Leu Phe Glu Leu Lys Leu Ala Glu Gly Asp Pro
244 305     310     315     320
247 Thr Thr Tyr Leu Val Asp Gly Thr Pro His Lys Met Thr Thr Arg Thr
248      325     330     335
251 Val Ala Phe Asp Val Lys Leu Pro Asp Gly Arg Leu Glu Arg Arg Thr
252      340     345     350
255 His Thr Phe Tyr Asp Thr Ile Tyr Gly Pro Val Leu Ser Met Pro Ser
256      355     360     365
259 Gly Gly Met Pro Trp Thr Thr Gln Lys Ala Tyr Ala Leu Arg Asp Ala
260      370     375     380
263 Asn Arg Asn Asn Thr Arg Ser Val Asp Ser Trp Leu His Ile Gly Gln
264 385     390     395     400
267 Ala Arg Asp Val Ala Gly Ile Arg Gln Ala Ile Gly Asn Leu Gly Ile
268      405     410     415
271 Pro Trp Val Asn Thr Ile Ala Thr Asp Arg Asn Gly Arg Ala Leu Phe

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272          420          425          430
275 Ala Asp Val Ser Thr Thr Pro Asp Val Pro Ala Ala Glu Leu Gln Arg
276          435          440          445
279 Cys Ala Pro Ser Pro Leu Ala Gly Lys Leu Phe Lys Asp Ala Gly Leu
280          450          455          460
283 Val Leu Leu Asp Gly Ser Arg Gly Thr Cys Asn Trp Gln Val Asp Pro
284 465          470          475          480
287 Ala Ser Pro Val Pro Gly Leu Val Ala Pro Ala Arg Met Pro Val Leu
288          485          490          495
291 Glu Arg Asp Asp Tyr Val Ala Asn Ser Asn Asp Ser Ser Trp Leu Thr
292          500          505          510
295 Asn Pro Ala Gln Lys Leu Thr Gly Phe Ser Pro Val Met Gly Ser Val
296          515          520          525
299 Asp Val Pro Gln Arg Leu Arg Thr Arg Ile Gly Leu Ile Glu Ile Gly
300          530          535          540
303 Arg Arg Leu Ala Gly Thr Asp Gly Leu Pro Gly Asn Arg Ile Asp Leu
304 545          550          555          560
307 Pro Asn Leu Gln Ala Met Ile Phe Ser Asn Ala Asn Leu Ala Gly Gln
308          565          570          575
311 Leu Val Leu Gly Asp Leu Leu Ala Ala Cys Lys Ala Thr Pro Ala Pro
312          580          585          590
315 Asp Ala Asp Val Arg Asp Gly Cys Ala Ala Leu Gly Gln Trp Asn Arg
316          595          600          605
319 Thr Ser Asn Ala Asp Ala Arg Ala Ala His Leu Phe Arg Glu Phe Trp
320          610          615          620
323 Met Arg Ala Lys Asp Ile Ala Gln Val His Ala Val Glu Phe Asp Pro
324 625          630          635          640
327 Ala Asp Pro Val His Thr Pro Arg Gly Leu Arg Met Asn Asp Ala Thr
328          645          650          655
331 Val Arg Thr Ala Val Phe Lys Ala Leu Lys Glu Ala Val Gly Ala Val
332          660          665          670
335 Arg Lys Ala Gly Phe Ala Leu Asp Ala Pro Leu Gly Thr Val Gln Ala
336          675          680          685
339 Ala His Ala Pro Asp Gly Ser Ile Ala Leu His Gly Gly Glu Glu Tyr
340          690          695          700
343 Glu Gly Val Leu Asn Lys Leu Gln Thr Leu Pro Ile Gly Pro Lys Gly
344 705          710          715          720
347 Leu Pro Val Tyr Phe Gly Thr Ser Tyr Ile Gln Thr Val Thr Phe Asp
348          725          730          735
351 Asp Gln Gly Pro Val Ala Asp Ala Ile Leu Thr Tyr Gly Glu Ser Thr
352          740          745          750
355 Asp His Ala Ser Pro His Ala Phe Asp Gln Met Arg Ala Tyr Ser Gly
356          755          760          765
359 Lys His Trp Asn Arg Leu Pro Phe Ser Glu Ala Ala Ile Ala Ala Asp
360          770          775          780
363 Pro Ala Leu Lys Val Met Arg Leu Ser Gln
364 785          790
367 <210> SEQ ID NO: 3
368 <211> LENGTH: 785

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369 <212> TYPE: PRT
370 <213> ORGANISM: Deinococcus radiodurans
372 <400> SEQUENCE: 3
374 Met Ser Arg Ser Pro Phe Ser Ser Val Ser Leu Pro Ala Arg Leu Leu
375 1 5 10 15
378 Leu Gly Ser Leu Leu Leu Gly Pro Leu Met Leu Gly Gly Ala Ala Ser
379 20 25 30
382 Ala Gln Thr Tyr Gln Val Gln Ile Gln Arg Thr Ala His Gly Ile Pro
383 35 40 45
386 His Ile Gln Ala Ser Asp Leu Gly Gly Ile Gly Tyr Gly Val Gly Tyr
387 50 55 60
390 Ser Tyr Ala Gln Asp Asn Leu Cys Leu Leu Ala Asp Gln Val Met Thr
391 65 70 75 80
394 Val Arg Gly Glu Arg Ser Lys Phe Leu Gly Ala Glu Gly Lys Thr Val
395 85 90 95
398 Val Gly Phe Gln Pro Val Asn Asn Leu Asp Ser Asp Val Phe Phe Lys
399 100 105 110
402 Thr Val Ile Glu Pro Gly Arg Leu Gln Ala Gly Tyr Arg Asp Gln Pro
403 115 120 125
406 Gln Ile Leu Ala Leu Met Arg Gly Tyr Val Ala Gly Val Asn Arg Tyr
407 130 135 140
410 Leu Arg Asp Thr Pro Pro Glu Gln Trp Pro Ser Ala Cys Arg Asn Ala
411 145 150 155 160
414 Asp Trp Val Arg Pro Leu Thr Glu Leu Asp Val Met Arg Leu Gly Glu
415 165 170 175
418 Glu Lys Ala Ile Gln Ala Ser Ala Gly Ala Met Val Ser Ala Ile Thr
419 180 185 190
422 Ser Ala Arg Pro Pro Gln Ala Gly Ala Ser Thr Ala Ala Pro Arg Pro
423 195 200 205
426 Asp Leu Ala Ala Phe Asn Arg Gln Tyr Arg Phe Asn Asp Leu Pro Ile
427 210 215 220
430 Gly Ser Asn Gly Trp Ala Phe Gly Ser Glu Ala Thr Thr Asn Gly Arg
431 225 230 235 240
434 Gly Leu Leu Leu Gly Asn Pro His Phe Pro Trp Glu Thr Ser Asn Arg
435 245 250 255
438 Phe Tyr Gln Leu His Leu Thr Leu Pro Gly Gln Phe Asp Val Met Gly
439 260 265 270
442 Ala Ser Leu Gly Gly Met Pro Val Val Asn Ile Gly Phe Asn Gln Asp
443 275 280 285
446 Val Ala Trp Thr His Thr Val Ser Thr Asp Lys Arg Phe Thr Leu Ala
447 290 295 300
450 Ala Leu Thr Leu Val Pro Gly Asp Pro Leu Ser Tyr Val Lys Asp Gly
451 305 310 315 320
454 Gln Gln Arg Arg Leu Gln Arg Arg Thr Ala Val Ile Glu Val Lys Thr
455 325 330 335
458 Ala Asn Gly Pro Arg Leu His Thr Arg Thr Val Tyr Phe Thr Pro Glu
459 340 345 350
462 Gly Pro Leu Val Asn Leu Pro Ala Ala Gly Leu Thr Trp Thr Pro Gln
463 355 360 365

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/502,351

DATE: 03/13/2005
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Input Set : A:\2977-154 Sequence Listing.ST25.txt
Output Set: N:\CRF4\03132005\J502351.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 16

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/502,351

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Input Set : A:\2977-154 Sequence Listing.ST25.txt

Output Set: N:\CRF4\03132005\J502351.raw

L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

L:999 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7